

C.

Axis number	Polarity
10	1
11	0.4
12	1
13	0.4
14	0.8
15	0.2
16	0.8
17	0.8
18	0.6
19	0.8
20	0.8
21	0.8
22	0.8
Average	0.708

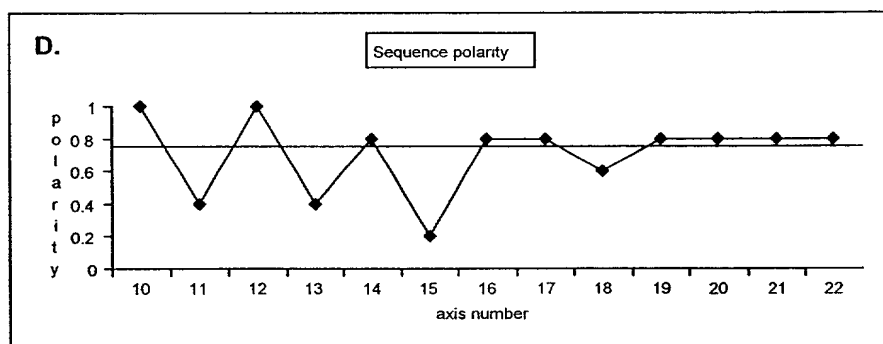
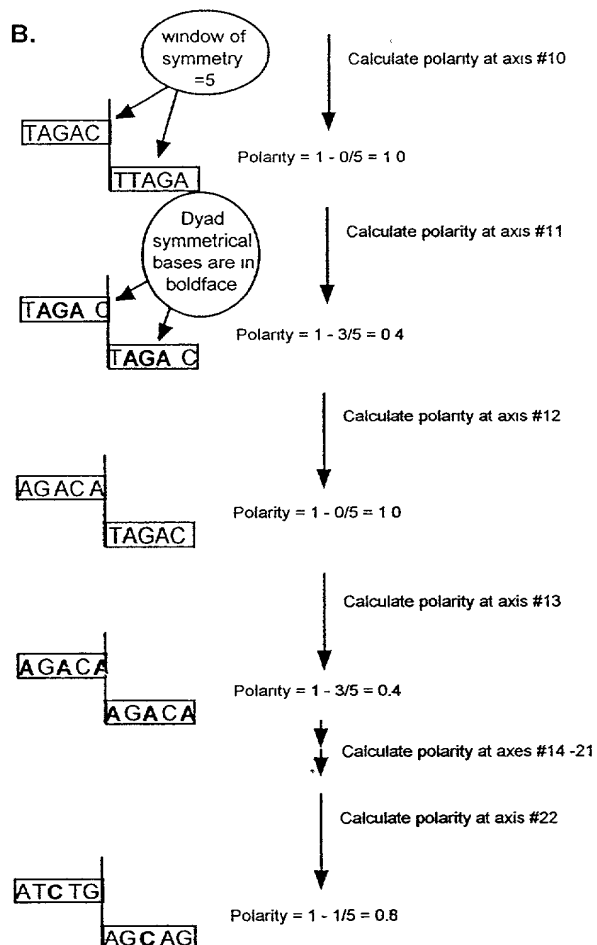


FIGURE 1

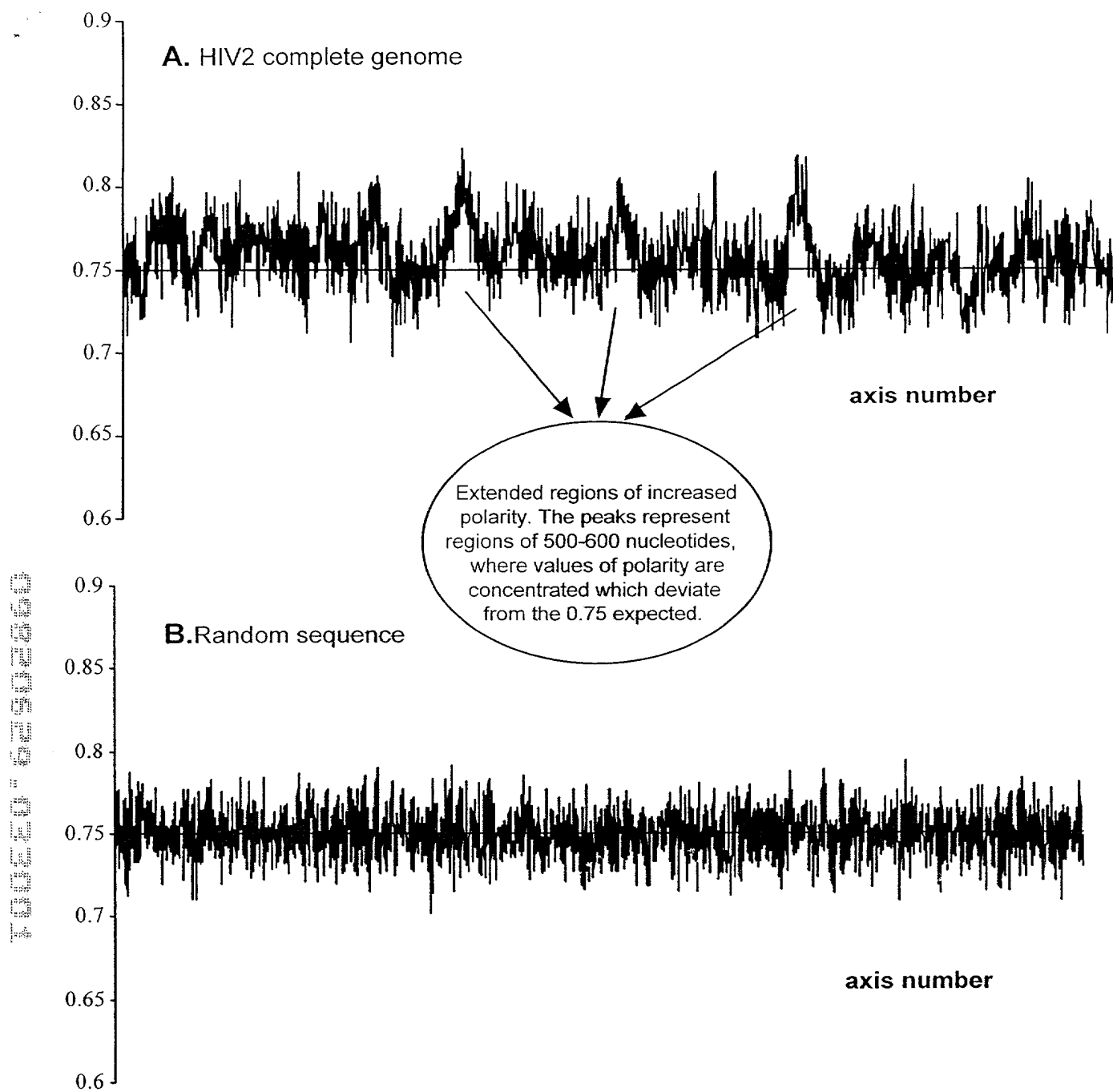
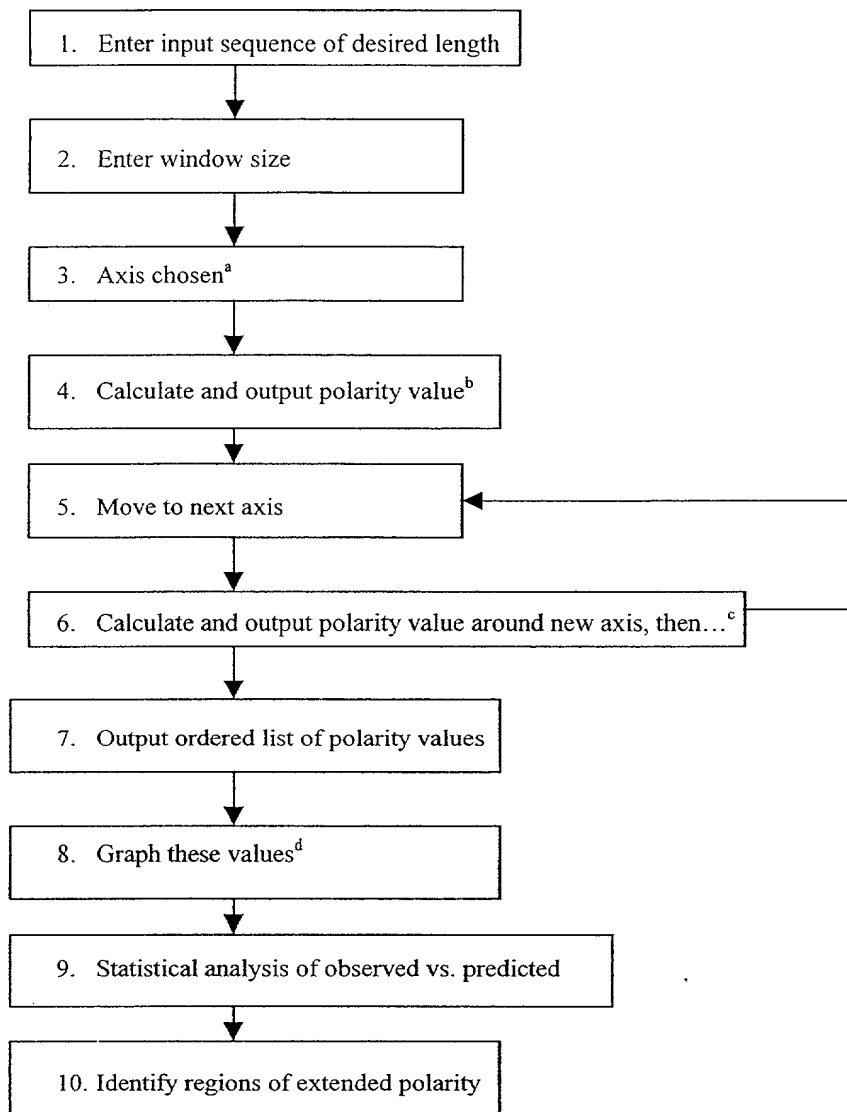


FIGURE 2



<sup>a</sup> Starting at position =  $(2 \times \text{window of symmetry})$

<sup>b</sup>  $[1 - (S/W)]$

<sup>c</sup> Up to and including axis position =  $[2 \times \text{length} - (2 \times \text{window size})]$

<sup>d</sup> Can use a moving average of values (with number of values averaged and increment of moving being variable) to smooth curve

FIGURE 3

The algorithm was implemented in PERL programming language  
 PERL variable-names and function-names are in boldface.

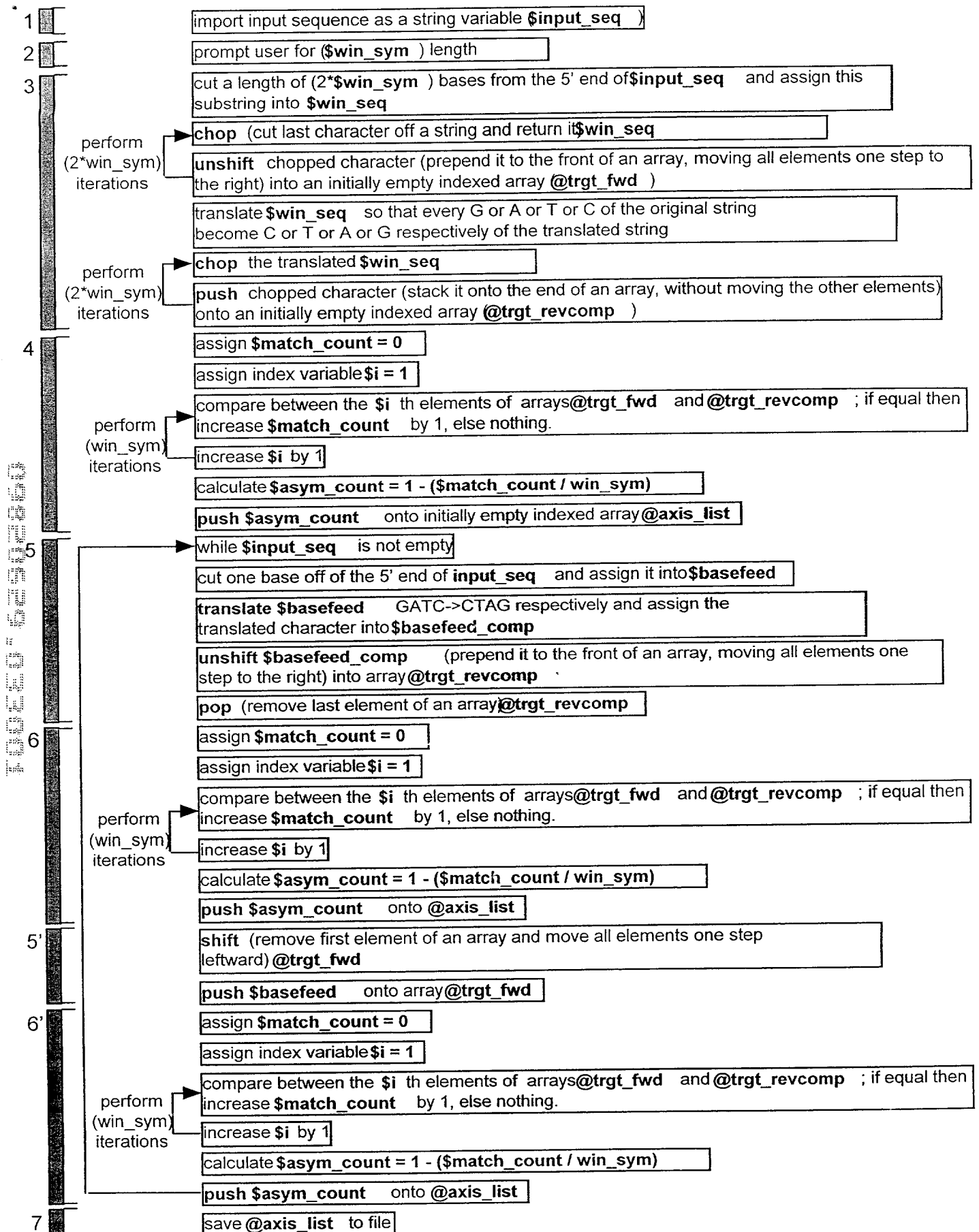
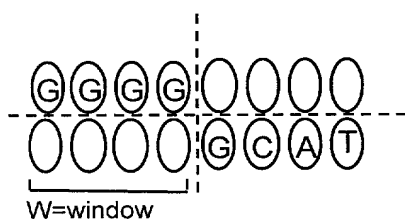


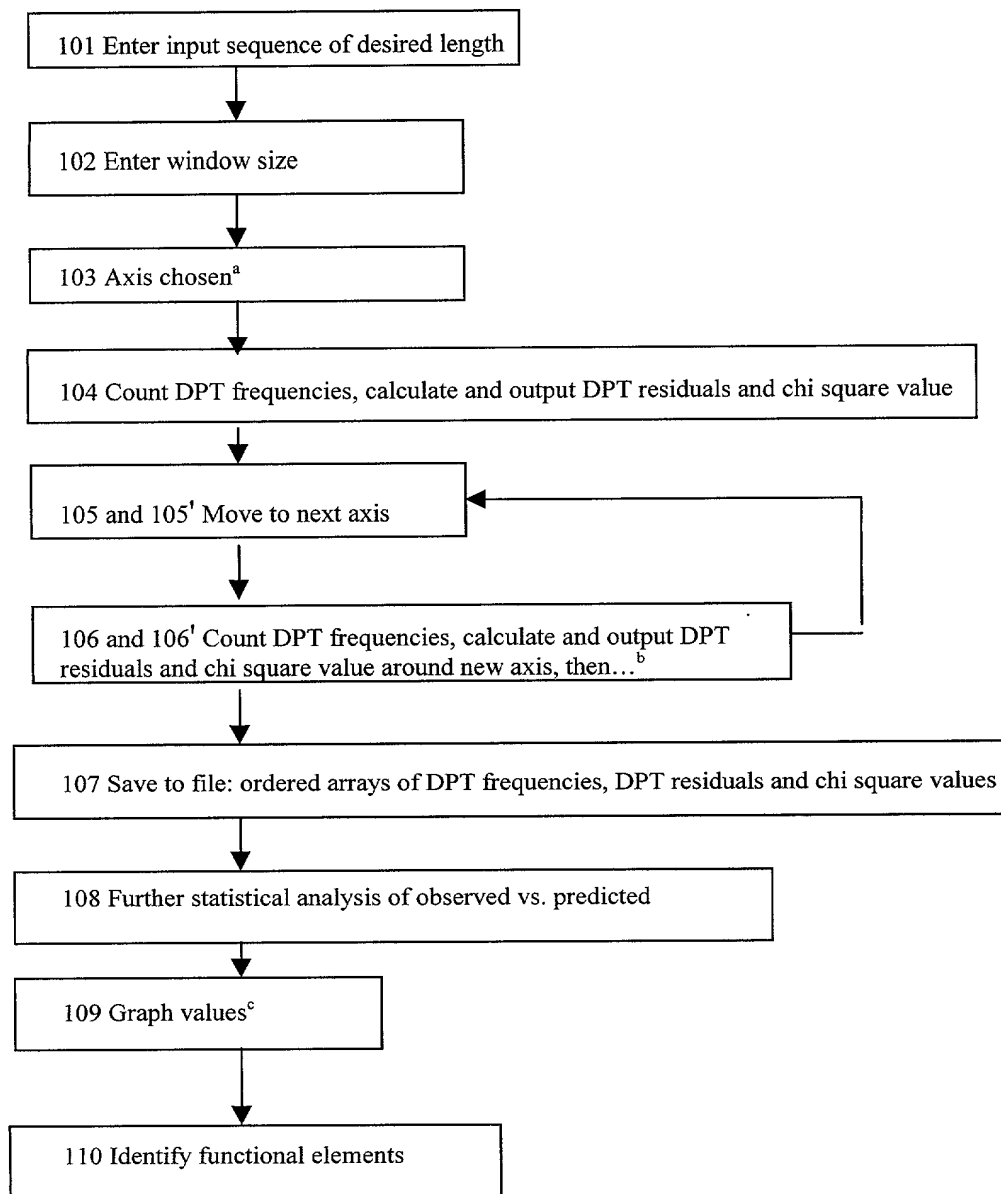
FIGURE 4

self dyad	self mirror	Purine pyrimidine dyad	Purine pyrimidine mirror
i=1: G--G	i=5: G--C	i=9: G--A	i=13: G--T
i=2: A--A	i=6: A--T	i=10: A--G	i=14: A--C
i=3: T--T	i=7: T--A	i=11: T--C	i=15: T--G
i=4: C--C	i=8: C--G	i=12: C--T	i=16: C--A

↑  
Figure 5A

Figure 5B





<sup>a</sup> Starting at axis position =  $(2 * \text{window size})$

<sup>b</sup> Up to and including axis position =  $[2 * \text{length} - (2 * \text{window size})]$

<sup>c</sup> Values include DPT frequencies, statistical measures including residuals and  $\chi^2$

FIGURE 6

The algorithm was implemented in PERL programming language.  
 PERL variable-names and function-names are in boldface.

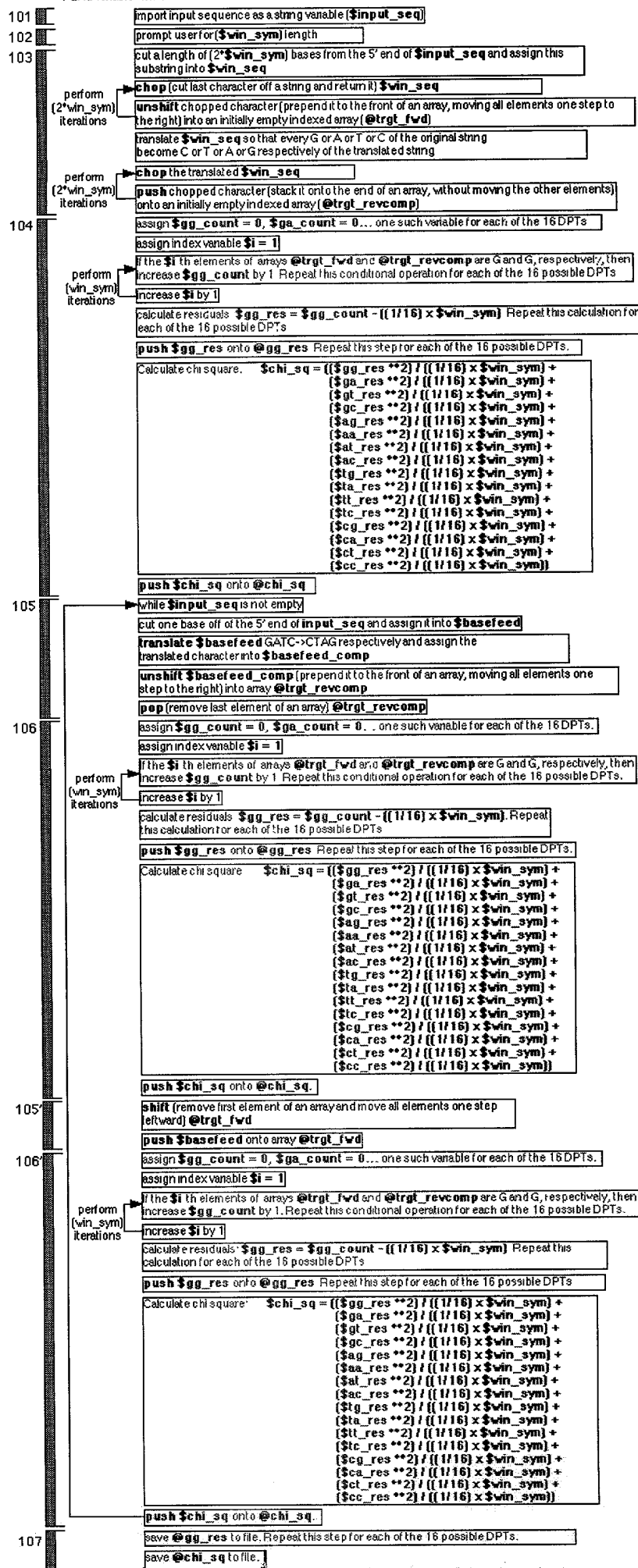


FIGURE 7

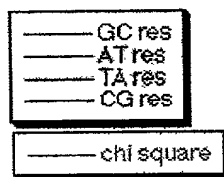


FIGURE 8



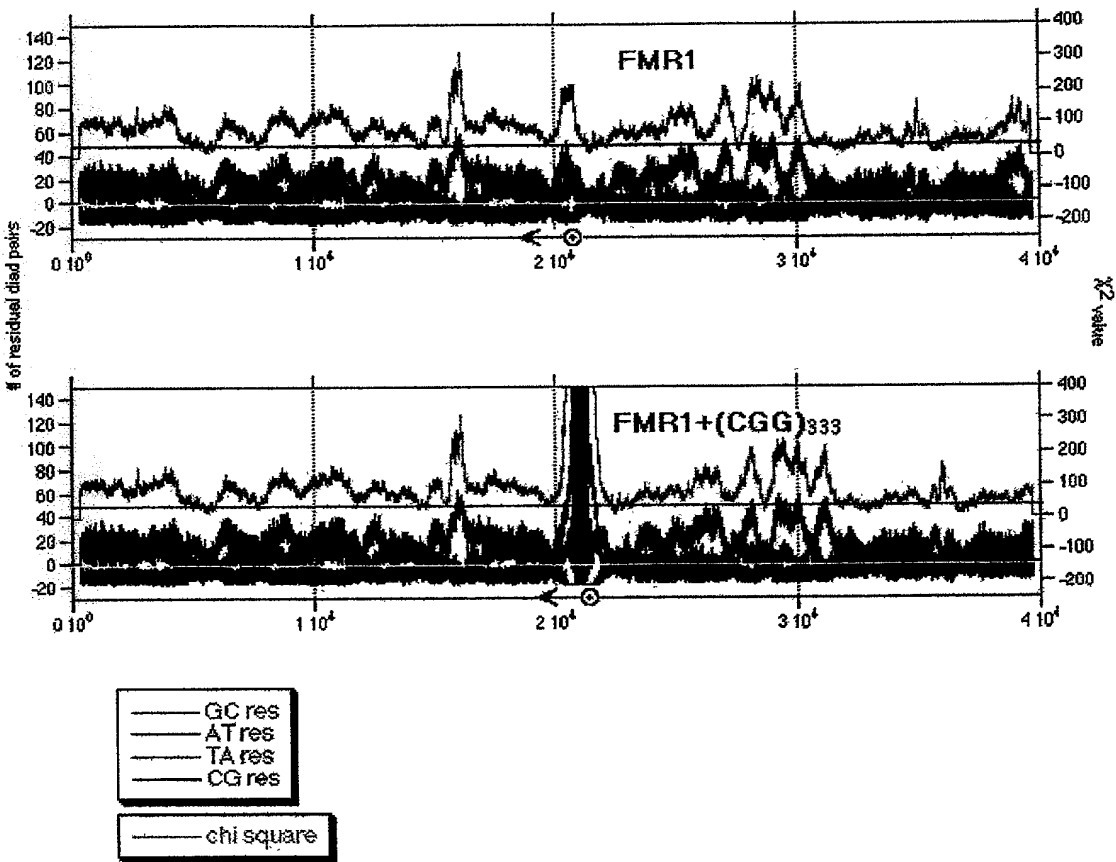


FIGURE 9

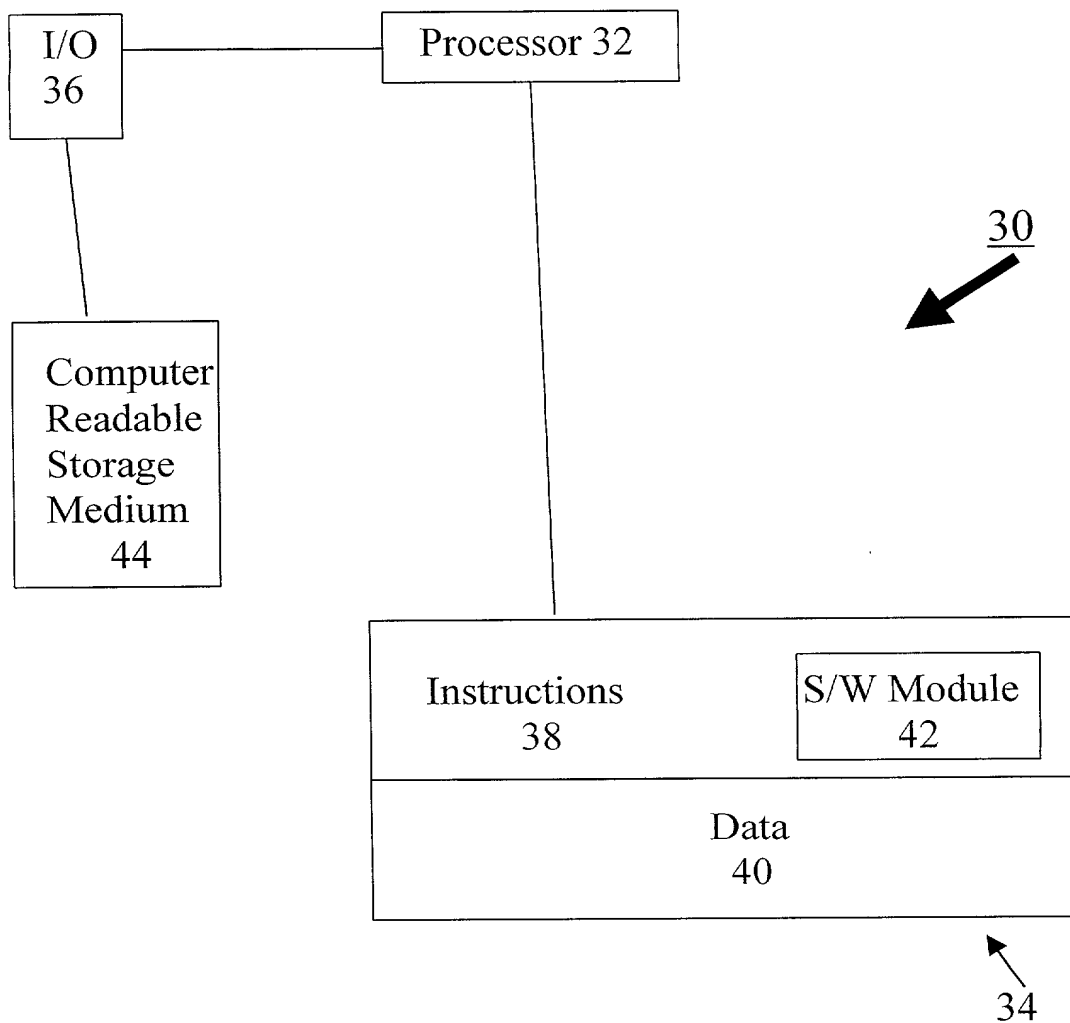


FIGURE 10